

SEQUENCE LISTING

<110> Sewalt, Vincent J. H.
Jung, Rudolf
Hu, Wang-Nan
Meeley, Robert B.

<120> Improved Grain Quality Through Altered
Expression of Seed Proteins

<130> 1276

<150> US 60/246,455

<151> 2000-11-07

<160> 10

<170> FastSEQ for Windows Version 3.0

<210> 1

<211> 1129

<212> DNA

<213> Zea mays

<220>

<221> CDS

<222> (120)...(1004)

<223> 50 kD gamma-zein prolamin/PTA 2272

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atg aag ctg gtg ctt gtg gtt ctt gct ttc att gct tta gta tca agt	167
Met Lys Leu Val Leu Val Val Leu Ala Phe Ile Ala Leu Val Ser Ser	
1 5 10 15	
ggt tct tgt aca cag aca ggc ggc tgc agc tgt ggt caa caa caa agc	215
Val Ser Cys Thr Gln Thr Gly Gly Cys Ser Cys Gly Gln Gln Gln Ser	
20 25 30	
cat gag cag caa cat cat cca caa caa cat cat cca caa aaa caa caa	263
His Glu Gln Gln His His Pro Gln Gln His His Pro Gln Lys Gln Gln	
35 40 45	
cat caa cca cca cca caa cat cac cag cag cag caa cac caa caa caa	311
His Gln Pro Pro Pro Gln His His Gln Gln Gln Gln His Gln Gln Gln	
50 55 60	
caa gtt cac atg caa cca caa aaa cat cag caa caa caa gaa gtt cat	359
Gln Val His Met Gln Pro Gln Lys His Gln Gln Gln Gln Glu Val His	
65 70 75 80	
ggt caa caa caa caa caa caa ccg cag cac caa caa caa caa caa caa	407
Val Gln Gln Gln Gln Gln Gln Pro Gln His Gln Gln Gln Gln Gln Gln	

85	90	95	
caa cag cac Gln Gln His 100	caa caa cat Gln Gln His 105	caa cag ggc Gln Gln Gln 110	455
caa caa tca Gln Gln Ser 115	caa ggc cat Gln Gly His 120	caa cag agc Gln Ser His 125	503
cac caa gga His Gln Gly 130	cag agc cat Gln Ser His 135	caa cag ggt Gln Gln Gln 140	551
cat gac aag His Asp Lys 145	cag caa cca Gln Gln Pro 150	caa tat cag Gln Tyr Gln 155	599
cag gaa aaa Gln Glu Lys 165	tca caa cag Ser Gln Gln 170	caa gag cag Gln Glu Gln 175	647
act aca agg Thr Thr Arg 180	tgc agc tat Cys Ser Tyr 185	aaa cta aaa Leu Lys 190	695
aat tgt cat Asn Cys His 195	gaa ttc cta Glu Phe Leu 200	agg cag cag Arg Gln Gln 205	743
ttt ctc caa Phe Leu Gln 210	tca cgt ttg Ser Arg Leu 215	ata caa cca Ile Gln Pro 220	791
caa caa tgt Gln Gln Cys 225	tgt cat gat Cys His Asp 230	agg cag att Arg Gln Ile 235	839
caa gca atc Gln Ala Ile 245	tac aac atg Tyr Asn Met 250	gag gag gag Pro Gln Glu 255	887
caa caa cca Gln Gln Pro 260	tgt gag tta Cys Glu Leu 265	tgt gga tct Gly Ser Gln 270	935
ggg ggc aat Gly Gly Asn 275	ctt gac agc Leu Asp Ser 280	aga ata cct Thr Ile Pro 285	983
gta cca ctc Val Pro Leu 290	ata cta cca Ile Leu Pro 295	aaa taatccatgc Lys 300	1034
tggtttgcaat ataaagtacc	tgaagaattg atacattatg	tgtctaccta atgttaaaaa	1094 1129

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 <212> PRT
 <213> Zea mays

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 His Glu Gln Gln His His Pro Gln Gln His His Pro Gln Lys Gln Gln
 35 40 45
 His Gln Pro Pro Pro Gln His His Gln Gln Gln Gln His Gln Gln Gln
 50 55 60
 Gln Val His Met Gln Pro Gln Lys His Gln Gln Gln Gln Glu Val His
 65 70 75 80
 Val Gln Gln Gln Gln Gln Gln Pro Gln His Gln Gln Gln Gln Gln Gln
 85 90 95
 Gln Gln His Gln Gln Gln His Gln Cys Glu Gly Gln Gln Gln His His
 100 105 110
 Gln Gln Ser Gln Gly His Val Gln Gln His Glu Gln Ser His Glu Gln
 115 120 125
 His Gln Gly Gln Ser His Glu Gln Gln His Gln Gln Gln Phe Gln Gly
 130 135 140
 His Asp Lys Gln Gln Gln Pro Gln Gln Pro Gln Gln Tyr Gln Gln Gly
 145 150 155 160
 Gln Glu Lys Ser Gln Gln Gln Gln Cys His Cys Gln Glu Gln Gln Gln
 165 170 175
 Thr Thr Arg Cys Ser Tyr Asn Tyr Tyr Ser Ser Ser Ser Asn Leu Lys
 180 185 190
 Asn Cys His Glu Phe Leu Arg Gln Gln Cys Ser Pro Leu Val Met Pro
 195 200 205
 Phe Leu Gln Ser Arg Leu Ile Gln Pro Ser Ser Cys Gln Val Leu Gln
 210 215 220
 Gln Gln Cys Cys His Asp Leu Arg Gln Ile Glu Pro Gln Tyr Ile His
 225 230 235 240
 Gln Ala Ile Tyr Asn Met Val Gln Ser Ile Ile Gln Glu Glu Gln Gln
 245 250 255
 Gln Gln Pro Cys Glu Leu Cys Gly Ser Gln Gln Ala Thr Pro Lys Cys
 260 265 270
 Gly Gly Asn Leu Asp Ser Ser Thr Ile Pro Thr Ile Asn Val Arg Leu
 275 280 285
 Val Pro Leu Ile Leu Pro Lys
 290 295

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<220>
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 <222> (111)...(728)
 <223> 18 kD alpha-globulin/PTA 2274

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acaagtggcg acagacaaag atttgtgagg gtgatccgcg ctgagaagag atg gct      116
                                     Met Ala
                                     1

aag atc gcc gcg gcg gcg gcg gcg gcg ctg tgc ttc gcg gcc ctg gtg      164
Lys Ile Ala Ala Ala Ala Ala Ala Ala Leu Cys Phe Ala Ala Leu Val
      5                      10                      15

gcc gtg gcc gtc tgc caa ggc gag gtc gag cgg cag agg ctc agg gac      212
Ala Val Ala Val Cys Gln Gly Glu Val Glu Arg Gln Arg Leu Arg Asp
      20                      25                      30

ctg cag tgc tgg cag gag gtc cag gag agc ccg ctc gac gcg tgc cgc      260
Leu Gln Cys Trp Gln Glu Val Gln Glu Ser Pro Leu Asp Ala Cys Arg
      35                      40                      45                      50

cag gtc ctc gac cgg cag cta acc ggc ggc ggc ggc ggc ggc ggc gtt      308
Gln Val Leu Asp Arg Gln Leu Thr Gly Gly Gly Gly Gly Gly Gly Val
      55                      60                      65

ggc ccg ttc cgg tgg ggc acc ggg ctc cgg atg cgg tgc tgc cag cag      356
Gly Pro Phe Arg Trp Gly Thr Gly Leu Arg Met Arg Cys Cys Gln Gln
      70                      75                      80

ctc cag gac gtg agc cgc gag tgc cgc tgc gcc gcc atc cgg agc atg      404
Leu Gln Asp Val Ser Arg Glu Cys Arg Cys Ala Ala Ile Arg Ser Met
      85                      90                      95

gtc agg ggc tac gag gag gcc atg ccg ccg ctg gag aaa ggc tgg tgg      452
Val Arg Gly Tyr Glu Glu Ala Met Pro Pro Leu Glu Lys Gly Trp Trp
      100                      105                      110

cca tgg ggg cgg cag cag cag ccg ccg ccg cag gga gga gga gga gga      500
Pro Trp Gly Arg Gln Gln Gln Pro Pro Pro Gln Gly Gly Gly Gly Gly
      115                      120                      125                      130

cag ggg ggc tac tac tac ccc tgc agc cgg cca gga gag gga tac ggc      548
Gln Gly Gly Tyr Tyr Tyr Pro Cys Ser Arg Pro Gly Glu Gly Tyr Gly
      135                      140                      145

tac ggt cag ggt ggc cag ccg cag atg tat cca ccg tgt cgt ccc ggc      596
Tyr Gly Gln Gly Gly Gln Arg Gln Met Tyr Pro Pro Cys Arg Pro Gly
      150                      155                      160

acc acc ggc ggc ggg cca agg atc ggc cgc gtg agg ctt acg aag gcc      644
Thr Thr Gly Gly Gly Pro Arg Ile Gly Arg Val Arg Leu Thr Lys Ala
      165                      170                      175

cgg gag tac gcc gcg ggg ttg ccg atg atg tgc cgg ctg tcg gag ccc      692
Arg Glu Tyr Ala Ala Gly Leu Pro Met Met Cys Arg Leu Ser Glu Pro
      180                      185                      190

cag gag tgc agc atc ttc tcc ggc ggc gac cag tac tagctaccat      738
Gln Glu Cys Ser Ile Phe Ser Gly Gly Asp Gln Tyr

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195 200 205

ggttaaagcg agtcggcgcg aggtgcaaga cgcagcatgt gtactgtgcg cgtgcaaatac 798
 cagaatgacg tagctctgac gtgggctcgc aatattgtcg cgtgttcggt acaataatga 858
 taataactat gaggaataaa tatgggaatg ttgccagata gtactggcgc cggttcttca 918
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aa 950

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 <212> PRT
 <213> Zea mays

<400> 4

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 Arg Asp Leu Gln Cys Trp Gln Glu Val Gln Glu Ser Pro Leu Asp Ala
 35 40 45
 Cys Arg Gln Val Leu Asp Arg Gln Leu Thr Gly Gly Gly Gly Gly
 50 55 60
 Gly Val Gly Pro Phe Arg Trp Gly Thr Gly Leu Arg Met Arg Cys Cys
 65 70 75 80
 Gln Gln Leu Gln Asp Val Ser Arg Glu Cys Arg Cys Ala Ala Ile Arg
 85 90 95
 Ser Met Val Arg Gly Tyr Glu Glu Ala Met Pro Pro Leu Glu Lys Gly
 100 105 110
 Trp Trp Pro Trp Gly Arg Gln Gln Gln Pro Pro Pro Gln Gly Gly Gly
 115 120 125
 Gly Gly Gln Gly Gly Tyr Tyr Tyr Pro Cys Ser Arg Pro Gly Glu Gly
 130 135 140
 Tyr Gly Tyr Gly Gln Gly Gly Gln Arg Gln Met Tyr Pro Pro Cys Arg
 145 150 155 160
 Pro Gly Thr Thr Gly Gly Gly Pro Arg Ile Gly Arg Val Arg Leu Thr
 165 170 175
 Lys Ala Arg Glu Tyr Ala Ala Gly Leu Pro Met Met Cys Arg Leu Ser
 180 185 190
 Glu Pro Gln Glu Cys Ser Ile Phe Ser Gly Gly Asp Gln Tyr
 195 200 205

<210> 5
 <211> 1679
 <212> DNA
 <213> Zea mays

<220>
 <221> CDS
 <222> (34)...(1485)
 <223> 50 kD legumin-1 prolamin/PTA 2273

<400> 5

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 Met Ala Ala Ala Ile Val Leu
 1 5

tcc ggc cag gtg cgg ccg ctt ccc tcg tcg ctg ccc ctg tcc ctg ctg 102

Ser	Gly	Gln	Val	Arg	Pro	Leu	Pro	Ser	Ser	Leu	Pro	Leu	Ser	Leu	Leu	
		10					15					20				
ctg	ctc	ctc	ctc	ctg	tgc	tgc	tcc	ggc	acc	tcg	tgg	gga	tgg	agc	acg	150
Leu	Leu	Leu	Leu	Leu	Cys	Cys	Ser	Gly	Thr	Ser	Trp	Gly	Trp	Ser	Thr	
	25					30				35						
tcc	cgg	gga	gga	gcc	gcc	agg	gag	tgc	ggc	ttc	gat	ggc	aag	ctg	gag	198
Ser	Arg	Gly	Gly	Ala	Ala	Arg	Glu	Cys	Gly	Phe	Asp	Gly	Lys	Leu	Glu	
	40				45				50					55		
gcc	ctg	gag	cgg	cgc	cac	aag	gtg	cag	tct	gag	gcc	ggc	tcc	gtc	cag	246
Ala	Leu	Glu	Pro	Arg	His	Lys	Val	Gln	Ser	Glu	Ala	Gly	Ser	Val	Gln	
				60				65						70		
tac	ttc	agc	cgg	ttc	aac	gaa	gcc	gac	cgg	gag	ctc	acc	tgc	gcc	ggc	294
Tyr	Phe	Ser	Arg	Phe	Asn	Glu	Ala	Asp	Arg	Glu	Leu	Thr	Cys	Ala	Gly	
			75				80						85			
atc	ttc	gcc	gtc	cgc	gtc	gtc	gtc	gac	gcc	atg	ggc	ctc	ctg	ctc	cct	342
Ile	Phe	Ala	Val	Arg	Val	Val	Val	Asp	Ala	Met	Gly	Leu	Leu	Leu	Pro	
		90					95					100				
cga	tac	tcc	aac	gtc	cat	tcg	ctt	gtc	tac	atc	gtc	caa	ggg	aga	ggg	390
Arg	Tyr	Ser	Asn	Val	His	Ser	Leu	Val	Tyr	Ile	Val	Gln	Gly	Arg	Gly	
	105					110					115					
atc	att	ggg	ttc	tcg	ttt	cgg	gga	tgc	caa	gag	gag	acc	cag	cag	cag	438
Ile	Ile	Gly	Phe	Ser	Phe	Pro	Gly	Cys	Gln	Glu	Glu	Thr	Gln	Gln	Gln	
	120				125				130					135		
cag	tat	gga	tac	gga	tat	gga	tat	gga	cac	cat	cac	cat	cag	cat	gac	486
Gln	Tyr	Gly	Tyr	Gly	Tyr	Gly	Tyr	Gly	His	His	His	His	Gln	His	Asp	
				140					145					150		
cac	cac	aag	atc	cac	cga	ttc	gag	cag	ggc	gac	gtg	gtg	gcc	atg	cgg	534
His	His	Lys	Ile	His	Arg	Phe	Glu	Gln	Gly	Asp	Val	Val	Ala	Met	Pro	
			155					160					165			
gcc	ggc	gcc	cag	cac	tgg	ctg	tac	aac	gac	ggc	gac	gcg	cgg	ctt	gtg	582
Ala	Gly	Ala	Gln	His	Trp	Leu	Tyr	Asn	Asp	Gly	Asp	Ala	Pro	Leu	Val	
		170					175					180				
gcy	gtc	tac	gtc	ttc	gac	gag	aac	aac	aac	atc	aac	cag	ctc	gag	cct	630
Ala	Val	Tyr	Val	Phe	Asp	Glu	Asn	Asn	Asn	Ile	Asn	Gln	Leu	Glu	Pro	
	185					190					195					
tcc	atg	agg	aaa	ttt	ttg	ctg	gct	ggg	ggc	ttc	agc	aag	ggg	cag	ccc	678
Ser	Met	Arg	Lys	Phe	Leu	Leu	Ala	Gly	Gly	Phe	Ser	Lys	Gly	Gln	Pro	
	200				205					210				215		
cac	ttc	gcc	gag	aac	atc	ttc	aaa	ggg	atc	gac	gcc	cgg	ttc	ctg	agc	726
His	Phe	Ala	Glu	Asn	Ile	Phe	Lys	Gly	Ile	Asp	Ala	Arg	Phe	Leu	Ser	
				220					225					230		
gaa	gcc	ctg	ggc	gtc	agc	atg	cac	gtc	gcc	gag	aag	ctg	cag	agc	cgg	774

Glu Ala Leu Gly Val Ser Met His Val Ala Glu Lys Leu Gln Ser Arg	
235 240 245	
cgt gac cag cga ggc gag atc gtc cgc gtg gag ccg gag cac ggc ttt	822
Arg Asp Gln Arg Gly Glu Ile Val Arg Val Glu Pro Glu His Gly Phe	
250 255 260	
cac cag ctg aat ccg tcg ccg tcg tcg tcg tcg ttt tcg ttc cca tcg	870
His Gln Leu Asn Pro Ser Pro Ser Ser Ser Ser Phe Ser Phe Pro Ser	
265 270 275	
tca caa gtc cag tac caa acg tgc cag cgc gac gtc gac agg cac aac	918
Ser Gln Val Gln Tyr Gln Thr Cys Gln Arg Asp Val Asp Arg His Asn	
280 285 290 295	
gtc tgc gcc atg gag gtg agg cac agc gtc gaa cgg ctg gac cag gcc	966
Val Cys Ala Met Glu Val Arg His Ser Val Glu Arg Leu Asp Gln Ala	
300 305 310	
gac gtc tac agc cct ggg gct ggg agg atc aca cgc ctc acc agc cac	1014
Asp Val Tyr Ser Pro Gly Ala Gly Arg Ile Thr Arg Leu Thr Ser His	
315 320 325	
aag ttc ccc gtc ctc aac ctc gta cag atg agc gcg gtg cgg gta gac	1062
Lys Phe Pro Val Leu Asn Leu Val Gln Met Ser Ala Val Arg Val Asp	
330 335 340	
ctg tac cag gac gcc atc atg tcg ccg ttc tgg aac ttc aac gcc cac	1110
Leu Tyr Gln Asp Ala Ile Met Ser Pro Phe Trp Asn Phe Asn Ala His	
345 350 355	
agc gcc atg tac ggc atc agg ggc agt gca agg gtc cag gtc gcc agc	1158
Ser Ala Met Tyr Gly Ile Arg Gly Ser Ala Arg Val Gln Val Ala Ser	
360 365 370 375	
gac aac ggg acc acg gtg ttc gac gac gtg ctc cgt gcg ggg cag ctg	1206
Asp Asn Gly Thr Thr Val Phe Asp Asp Val Leu Arg Ala Gly Gln Leu	
380 385 390	
ctc atc gta ccc cag ggc tac ctc gtc gcc acc aag gcg cag gga gaa	1254
Leu Ile Val Pro Gln Gly Tyr Leu Val Ala Thr Lys Ala Gln Gly Glu	
395 400 405	
ggc ttc cag tac atc gcc ttc gag acg aac cct gac acc atg gtc agc	1302
Gly Phe Gln Tyr Ile Ala Phe Glu Thr Asn Pro Asp Thr Met Val Ser	
410 415 420	
cac gtc gcc ggg aag aac tcc gtc ctg agc gac ttg ccg gcc gcc gtc	1350
His Val Ala Gly Lys Asn Ser Val Leu Ser Asp Leu Pro Ala Ala Val	
425 430 435	
atc gcc agc tcg tat gcc atc tcc atg gag gaa gct gca gag ctc aag	1398
Ile Ala Ser Ser Tyr Ala Ile Ser Met Glu Glu Ala Ala Glu Leu Lys	
440 445 450 455	
aac ggt agg aag cat gag ctg gct gtg ctt act cct gct ggc agt ggc	1446

Asn Gly Arg Lys His Glu Leu Ala Val Leu Thr Pro Ala Gly Ser Gly
460 465 470

agc tac caa caa ggt caa gct ggc agc gcc caa cag tag gcacaacctc 1495
Ser Tyr Gln Gln Gly Gln Ala Gly Ser Ala Gln Gln *
475 480

agagtgatct gcctgaataa gtactcgtag actgtaataa ttaaacaag cttgctcatg 1555
gttaaactgc gtgttgatta gtctttcaac tacatagctc taaagttttt gatacaccga 1615
gtgatttgcc agggaaaaaa tgagcagatt gttgtaagca aaaaaaaaaa aaaaaaaaaa 1675
aaaa 1679

<210> 6
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<212> PRT
<213> Zea mays

<400> 6

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35 40 45
Gly Phe Asp Gly Lys Leu Glu Ala Leu Glu Pro Arg His Lys Val Gln
50 55 60
Ser Glu Ala Gly Ser Val Gln Tyr Phe Ser Arg Phe Asn Glu Ala Asp
65 70 75 80
Arg Glu Leu Thr Cys Ala Gly Ile Phe Ala Val Arg Val Val Val Asp
85 90 95
Ala Met Gly Leu Leu Leu Pro Arg Tyr Ser Asn Val His Ser Leu Val
100 105 110
Tyr Ile Val Gln Gly Arg Gly Ile Ile Gly Phe Ser Phe Pro Gly Cys
115 120 125
Gln Glu Glu Thr Gln Gln Gln Gln Tyr Gly Tyr Gly Tyr Gly Tyr Gly
130 135 140
His His His His Gln His Asp His His Lys Ile His Arg Phe Glu Gln
145 150 155 160
Gly Asp Val Val Ala Met Pro Ala Gly Ala Gln His Trp Leu Tyr Asn
165 170 175
Asp Gly Asp Ala Pro Leu Val Ala Val Tyr Val Phe Asp Glu Asn Asn
180 185 190
Asn Ile Asn Gln Leu Glu Pro Ser Met Arg Lys Phe Leu Leu Ala Gly
195 200 205
Gly Phe Ser Lys Gly Gln Pro His Phe Ala Glu Asn Ile Phe Lys Gly
210 215 220
Ile Asp Ala Arg Phe Leu Ser Glu Ala Leu Gly Val Ser Met His Val
225 230 235 240
Ala Glu Lys Leu Gln Ser Arg Arg Asp Gln Arg Gly Glu Ile Val Arg
245 250 255
Val Glu Pro Glu His Gly Phe His Gln Leu Asn Pro Ser Pro Ser Ser
260 265 270
Ser Ser Phe Ser Phe Pro Ser Ser Gln Val Gln Tyr Gln Thr Cys Gln
275 280 285
Arg Asp Val Asp Arg His Asn Val Cys Ala Met Glu Val Arg His Ser
290 295 300

Val Glu Arg Leu Asp Gln Ala Asp Val Tyr Ser Pro Gly Ala Gly Arg
 305 310 315 320
 Ile Thr Arg Leu Thr Ser His Lys Phe Pro Val Leu Asn Leu Val Gln
 325 330 335
 Met Ser Ala Val Arg Val Asp Leu Tyr Gln Asp Ala Ile Met Ser Pro
 340 345 350
 Phe Trp Asn Phe Asn Ala His Ser Ala Met Tyr Gly Ile Arg Gly Ser
 355 360 365
 Ala Arg Val Gln Val Ala Ser Asp Asn Gly Thr Thr Val Phe Asp Asp
 370 375 380
 Val Leu Arg Ala Gly Gln Leu Leu Ile Val Pro Gln Gly Tyr Leu Val
 385 390 395 400
 Ala Thr Lys Ala Gln Gly Glu Gly Phe Gln Tyr Ile Ala Phe Glu Thr
 405 410 415
 Asn Pro Asp Thr Met Val Ser His Val Ala Gly Lys Asn Ser Val Leu
 420 425 430
 Ser Asp Leu Pro Ala Ala Val Ile Ala Ser Ser Tyr Ala Ile Ser Met
 435 440 445
 Glu Glu Ala Ala Glu Leu Lys Asn Gly Arg Lys His Glu Leu Ala Val
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 Leu Thr Pro Ala Gly Ser Gly Ser Tyr Gln Gln Gly Gln Ala Gly Ser
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 Ala Gln Gln

<210> 7
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 <212> DNA
 <213> Zea mays

<220>
 <221> allele
 <222> (0)...(0)
 <223> 50kD gamma-zein, B73 partial

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 acaacagcac caacaacaac atcaatgtga aggccaacaa caacatcacc aacaatcaca 180
 aggccatgtg caacaacacg aacagagcca tgagcaacac caaggacaga gccatgagca 240
 acaacatcaa caacaattcc aggggtcatga caagcagcaa caaccacaac agcctcagca 300
 atatcagcag ggccaggaaa aatc 324

<210> 8
 <211> 321
 <212> DNA
 <213> Zea mays

<220>
 <221> allele
 <222> (0)...(0)
 <223> 50kD gamma-zein, Mol7 partial

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 acaagaagtt catgttcaac aacaacaaca acaaccgcag caccaacaac aacaacaaca 120

acagcaccaa	caacaacatc	aatgtgaagg	ccaacaacaa	catcaccaac	aatcacaagg	180
ccatgtgcaa	caacacgaac	agagccatga	gcaacaccaa	ggacagagcc	atgagcaaca	240
acatcaacaa	caattccagg	gtcatgacaa	gcagcaacaa	ccacaacagc	ctcagcaata	300
tcagcagggc	caggaaaaat	c				321

<210> 9
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 <212> DNA
 <213> Zea mays

<220>
 <221> allele
 <222> (0)...(0)
 <223> 18 kD alpha-globulin, B73, partial

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ctcctggggc	tccgacagcc	ggcacatcat	cggcaacccc	gcccgcgtact	cccgggcctt	180
cgtaagcctc	acgcggccga	tccttgccc	gccgcgggtg	gtgccgggac	gacacgggtg	240
atacatctgc	cgctggccac	cctgaccgta	gocgtatccc	tctcctggcc	ggctgcaggg	300
gtagtagtag	ccccctgtc	ctcctcctcc	tccctgcggc	ggcggctgct	gctgccgccc	360
ccatggccac	cagcctttct	ccagcggcgg	catggcctcc	tcgtagcccc	tgaccatgct	420
ccggatggcg	gcgcagcggc	actcgcggct	cacgtcctgg	agctgctggc	agcaccgcat	480
ccggagcccc	gtgccccacc	ggaacggggc	aacgcgcgcg	ccgccgccgc	cgccgggttag	540
ctgccggctc	aggaaagggc	g				561

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 <212> DNA
 <213> Zea mays

<220>
 <221> allele
 <222> (0)...(0)
 <223> 18 kD alpha-globulin, Mol7 partial

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gatgctgcac	tcctggggct	ccgacagccg	gcacatcatc	ggcaaccccg	cggcgctactc	180
ccgggccttc	gtaagcctca	cgcggccgat	ccttgggccc	gtggtgccgg	gacgacacgg	240
tggtatcatc	tgcgttttgt	atccctctcc	tgcgcggctg	caggggtagt	agtagcccc	300
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